

ABSTRACT

An object of this invention is to provide a method for assaying, predicting or assessing drug metabolism by effectively detecting (a) mutation(s) in a gene coding for UGT. A gene coding for UGT comprises 5 exons, and since the regions of exons 2 through 5 are common to each isoform of UGT1, by assaying a mutation in the common regions, particularly a mutation in exon 5 region, and further adding the detection of (a) mutation(s) in a plurality of exon regions, mutations of UGT1 gene can effectively assayed. A nucleic acid chip using nucleic acid probes is used as a way of detecting (a) mutation(s).